

Seq ID 1001

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
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- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4635	100.0	4635	6	AAD39663	Aad39663 Human pho
2	4635	100.0	4635	13	ADQ89085	Adq89085 Human uro
3	3684.6	79.5	4237	6	ABA96005	Aba96005 Human lip
4	3345.2	72.2	4941	6	ABV72132	Abv72132 Nucleotid
5	2838.4	61.2	6551	6	ABK12390	Abk12390 cDNA enco
6	2838.4	61.2	6551	12	ADK70341	Adk70341 Respirato
7	2358	50.9	5365	13	ABD33214	Abd33214 Murine ca
8	2161.4	46.6	2243	6	ABA94696	Aba94696 Human lip
9	1540.4	33.2	6946	10	ADL15056	Adl15056 Human mal
10	1412.6	30.5	1833	13	ABD33216	Abd33216 Human c

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	4635	100.0	4635	2	AR658532	AR658532 Sequence
2	3922	84.6	6453	5	AK122589	AK122589 Homo sapi
3	3684.6	79.5	4237	2	AX304472	AX304472 Sequence
4	3624	78.2	3624	2	AR658533	AR658533 Sequence
5	3345.2	72.2	4941	2	AX512952	AX512952 Sequence
6	3339.2	72.0	5450	5	AB007919	AB007919 Homo sapi
7	2838.8	61.2	4837	5	DQ176850	DQ176850 Homo sapi
8	2838.4	61.2	6551	2	AX392826	AX392826 Sequence
9	2573.2	55.5	3497	6	AY966876	AY966876 Mus muscu
10	2527.4	54.5	4411	5	AK074149	AK074149 Homo sapi
11	2501.8	54.0	5333	6	AK129147	AK129147 Mus muscu
12	2297	49.6	4001	5	BC043358	BC043358 Homo sapi

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4635	100.0	4635	3	US-09-927-112-1	Sequence 1, Appli
2	3624	78.2	3624	3	US-09-927-112-3	Sequence 3, Appli
3	308.6	6.7	2289	3	US-10-258-860-1	Sequence 1, Appli
4	301.8	6.5	2211	3	US-09-800-971-3	Sequence 3, Appli
5	301.8	6.5	3425	3	US-09-800-971-1	Sequence 1, Appli
6	289.8	6.3	2627	4	US-09-880-107-3293	Sequence 3293, Ap
7	286.6	6.2	2752	3	US-10-104-047-135	Sequence 135, App
8	278.8	6.0	2627	3	US-09-949-016-5110	Sequence 5110, Ap
9	276.2	6.0	2462	3	US-10-258-860-5	Sequence 5, Appli
10	276.2	6.0	2540	3	US-10-258-860-3	Sequence 3, Appli
11	212.8	4.6	2958	3	US-09-688-078-5	Sequence

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4635	100.0	4635	3	US-09-927-112-1	Sequence 1, Appli
2	4635	100.0	4635	9	US-10-757-262-37	Sequence 37, Appl
3	4635	100.0	4635	9	US-10-784-089-1	Sequence 1, Appli
4	3684.6	79.5	4237	8	US-10-275-998-10	Sequence 10, Appl
5	3624	78.2	3624	3	US-09-927-112-3	Sequence 3, Appli
6	3624	78.2	3624	9	US-10-784-089-3	Sequence 3, Appli
7	3345.2	72.2	4941	8	US-10-467-248-15	Sequence 15, Appl
8	2838.4	61.2	6551	8	US-10-362-628-12	Sequence 12, Appl
9	2358	50.9	5365	8	US-10-322-281-224	Sequence 224, App
10	2161.4	46.6	2243	8	US-10-332-426-10	Sequence 10, Appl
11	1412.6	30.5	1833	8	US-10-322-281-227	Sequence 227, App
12	1127	24.3	3283	7	US-10-108-260A-1395	Sequence 1395, Ap
13	1111.2	24.0	3433	8	US-10-398-663-9	Sequence 9, Appli

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2358	50.9	5365	6	US-10-539-228-224	Sequence 224, App
2	1412.6	30.5	1833	6	US-10-539-228-227	Sequence 227, App
3	1127	24.3	3283	8	US-11-293-697-1395	Sequence 1395, Ap
4	1103	23.8	3585	8	US-11-266-748A-32259	Sequence 32259, A
5	571.2	12.3	715	8	US-11-266-748A-366378	Sequence 366378,
c 6	571.2	12.3	715	8	US-11-266-748A-449757	Sequence 449757,
7	535.4	11.6	80105	6	US-10-539-228-223	Sequence 223, App
c 8	464.4	10.0	513	8	US-11-266-748A-104368	Sequence 104368,
9	464.4	10.0	513	8	US-11-266-748A-157179	Sequence 157179,
10	308.6	6.7	3107	8	US-11-266-748A-30946	Sequence 30946, A
11	308.6	6.7	3107	8	US-11-266-748A-56285	Sequence 56285, A
12	301.8	6.5	3445	8	US-11-266-748A-28175	Sequence 28175, A
13	301.8	6.5	5926	8	US-11-266-748A-22592	Sequence 22592, A
14	300.2	6.5	2773	8	US-11-266-748A-57630	Sequence 57630

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- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
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- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query			Description
	Score	Match	Length	DB	ID	
1	2548	55.0	5324	6	AK044619	AK044619 Mus muscu
2	1307.6	28.2	1836	6	AK049970	AK049970 Mus muscu
3	1170.6	25.3	1817	6	AK078731	AK078731 Mus muscu
4	920.2	19.9	947	14	DQ035829	DQ035829 Homo sapi
5	808	17.4	1278	14	DQ035827	DQ035827 Homo sapi
6	717.4	15.5	857	14	DQ035830	DQ035830 Pan trogl
7	693.8	15.0	886	10	DV878798	DV878798 LB0263.CR
8	669.2	14.4	692	8	CR998048	CR998048 CR998048
9	647	14.0	889	3	BQ946757	BQ946757 AGENCOURT
10	644.6	13.9	958	3	BU159213	BU159213 AGENCOURT
11	627	13.5	759	5	CF531476	CF531476 UI-M-FY0-
12	626.6	13.5	763	5	CF531795	CF531795 UI-M-FY0-
13	620	13.4	1092	3	BU502871	BU502871 AGENCOURT

Seq ID No: 3

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
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- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	3624	100.0	3624	2	AR658533	AR658533 Sequence
2	3624	100.0	4635	2	AR658532	AR658532 Sequence
3	3360.2	92.7	6453	5	AK122589	AK122589 Homo sapi
4	3345.2	92.3	4941	2	AX512952	AX512952 Sequence
5	3339.2	92.1	5450	5	AB007919	AB007919 Homo sapi
6	3269.2	90.2	4237	2	AX304472	AX304472 Sequence
7	2838.8	78.3	4837	5	DQ176850	DQ176850 Homo sapi
8	2838.4	78.3	6551	2	AX392826	AX392826 Sequence
9	2573.2	71.0	3497	6	AY966876	AY966876 Mus muscu
10	2501.8	69.0	5333	6	AK129147	AK129147 Mus muscu
11	2297	63.4	4001	5	BC043358	BC043358 Homo sapi
12	2265.4	62.5	4791	6	DQ176851	DQ176851 Mus muscu
13	1965.6	54.2	4411	5	AK074149	AK074149 Homo sapi
14	1914.4	52.8	2697	2	CQ721801	CQ721801 Sequence
15	1840	50.8	2243	2	AX402958	AX402958

RESULT 7

DQ176850

LOCUS DQ176850 4837 bp mRNA linear PRI 18-SEP-2005

DEFINITION Homo sapiens phospholipase C-eta2 (PLC-eta2) mRNA, complete cds.

ACCESSION DQ176850

VERSION DQ176850.1 GI:74486662

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 4837)

AUTHORS Zhou, Y., Wing, M.R., Sondek, J. and Harden, T.K.

TITLE Molecular cloning and characterization of phospholipase C-eta2

JOURNAL (er) Biochem. J. (2005) In press

REFERENCE 2 (bases 1 to 4837)

AUTHORS Zhou, Y., Wing, M.R., Sondek, J. and Harden, T.K.

TITLE Direct Submission

JOURNAL Submitted (23-AUG-2005) Pharmacology, UNC Chapel Hill, 1106 ME
Jones Building (CB#7365), Chapel Hill, NC 27599, USA

FEATURES Location/Qualifiers

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/gene="PLC-eta2"

5'UTR

1. .274

/gene="PLC-eta2"

CDS

275. .4525

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3' UTR

4526. .4837

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ORIGIN

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Matches 2840; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	166	GGCGGCTCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGC	225
Db	452	GGCGGCTCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGC	511
Qy	226	TGGAGGCCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTG	285
Db	512	TGGAGGCCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTG	571
Qy	286	AGTGAGGGGCGGCAGTCGGAGGTC TTCCAGCGCTACCCTGACGGCAGCTTCGACCCCAAC	345
Db	572	AGTGAGGGGCGGCAGTCGGAGGTC TTCCAGCGCTACCCTGACGGCAGCTTCGACCCCAAC	631
Qy	346	TGCTGCTTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAGC	405
Db	632	TGCTGCTTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAGC	691
Qy	406	AGCGAGGTGGCGCGCACCTGGGTCACTGGCCTGCGCTACCTCATGGCCGGCATCAGCGAC	465
Db	692	AGCGAGGTGGCGCGCACCTGGGTCACTGGCCTGCGCTACCTCATGGCCGGCATCAGCGAC	751
Qy	466	GAGGACAGCCTGGCTCGCCGCCAGCGCACCAGGGACCAGTGGCTGAAGCAGACGTTTGAC	525
Db	752	GAGGACAGCCTGGCTCGCCGCCAGCGCACCAGGGACCAGTGGCTGAAGCAGACGTTTGAC	811
Qy	526	GAGGCCGACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTTGAGCTGCTGCAC	585
Db	812	GAGGCCGACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTTGAGCTGCTGCAC	871
Qy	586	AAGCTCAACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTT CAGGGAAGCGGACACG	645
Db	872	AAGCTCAACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTT CAGGGAAGCGGACACG	931
Qy	646	GATGACCACCAAGGGACGCTGGGTTTTGAAGAGTTCTGTGCCTTCTACAAGATGATGTCC	705
Db	932	GATGACCACCAAGGGACGCTGGGTTTTGAAGAGTTCTGTGCCTTCTACAAGATGATGTCC	991
Qy	706	ACCCGCCGGGACCTCTACCTGCTCATGCTGACCTACAGCAACCACAAGGACCACCTGGAT	765
Db	992	ACCCGCCGGGACCTCTACCTGCTCATGCTGACCTACAGCAACCACAAGGACCACCTGGAT	1051
Qy	766	GCCGCCAGCCTGCAGCGCTTCCTGCAGGTGGAGCAGAAGATGGCGGGTGTGACCCTCGAG	825
Db	1052	GCCGCCAGCCTGCAGCGCTTCCTGCAGGTGGAGCAGAAGATGGCGGGTGTGACCCTCGAG	1111

Qy	826	AGCTGCCAGGACATCATCGAGCAGTTTGAGCCATGCCAGAAAAAAGAGTAAGGGGCTG	885
Db	1112	AGCTGCCAGGACATCATCGAGCAGTTTGAGCCATGCCAGAAAAAAGAGTAAGGGGCTG	1171
Qy	886	CTGGGCATTGATGGCTTACCAACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCCT	945
Db	1172	CTGGGCATTGATGGCTTACCAACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCCT	1231
Qy	946	GAGCACCACCATGTGCAACCAGGACATGACGCAGCCGCTGAGCCACTACTTCATCACCTCG	1005
Db	1232	GAGCACCACCATGTGCAACCAGGACATGACGCAGCCGCTGAGCCACTACTTCATCACCTCG	1291
Qy	1006	TCCCACAACACCTACCTCGTGGGTGACCAGCTCATGTCCCAGTCACGGGTGGACATGTAT	1065
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Qy	1066	GCTTGGGTCCTGCAGGCTGGCTGCCGCTGCGTGGAGGTGGACTGCTGGGATGGGCCCCGAC	1125
Db	1352	GCTTGGGTCCTGCAGGCTGGCTGCCGCTGCGTGGAGGTGGACTGCTGGGATGGGCCCCGAC	1411
Qy	1126	GGGGAGCCCATTTGTGCACCATGGCTA CACTCTGACTTCCAAGATCCTCTTCAAAGACGTC	1185
Db	1412	GGGGAGCCCATTTGTGCACCATGGCTA CACTCTGACTTCCAAGATCCTCTTCAAAGACGTC	1471
Qy	1186	ATTGAAACCATCAACAAATATGCCTTCATCAAGAATGAGTACCCAGTGATCCTGTCCATC	1245
Db	1472	ATTGAAACCATCAACAAATATGCCTTCATCAAGAATGAGTACCCAGTGATCCTGTCCATC	1531
Qy	1246	GAAAACCACTGCAGTGT CATCCAGCAGAAGAAAATGGCCAGTATCTGACTGACATCCTT	1305
Db	1532	GAAAACCACTGCAGTGT CATCCAGCAGAAGAAAATGGCCAGTATCTGACTGACATCCTT	1591
Qy	1306	GGGGACAAGCTGGACCTGT CATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCCA	1365
Db	1592	GGGGACAAGCTGGACCTGT CATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCCA	1651
Qy	1366	CAGATGCTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCCAGCCAACATCAGCGAG	1425
Db	1652	CAGATGCTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCCAGCCAACATCAGCGAG	1711
Qy	1426	GATGCGGAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGACTGC	1485
Db	1712	GATGCGGAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGACTGC	1771
Qy	1486	AAGCTCCTCAATGGGGATGCATCCACCAATCGAAAGCGTGTAGAAAACACTGCTAAGAGG	1545
Db	1772	AAGCTCCTCAATGGGGATGCATCCACCAATCGAAAGCGTGTAGAAAACACTGCTAAGAGG	1831
Qy	1546	AAACTGGATTCCCTCATCAAAGAGTCGAAGATTCGGGACTGTGAGGACCCCAACAACCTTC	1605
Db	1832	AAACTGGATTCCCTCATCAAAGAGTCGAAGATTCGGGACTGTGAGGACCCCAACAACCTTC	1891
Qy	1606	TCCGTCTCCACACTGTCCCATCTGGAAGCTCGGACGCAAGAGCAAGGCTGAAGAGGAC	1665
Db	1892	TCCGTCTCCACACTGTCCCATCTGGAAGCTCGGACGCAAGAGCAAGGCTGAAGAGGAC	1951
Qy	1666	GTGGAGTCTGGGGAGGATGCCGGGGCCAGCAGACGCAATGGCCGCCTCGTCGTGGGAAGC	1725
Db	1952	GTGGAGTCTGGGGAGGATGCCGGGGCCAGCAGACGCAATGGCCGCCTCGTCGTGGGAAGC	2011
Qy	1726	TTCTCCAGGCGCAAGAAGAAGGGCAGCAAGCTGAAGAAGGCGCCAGCGTGGAGGAGGGA	1785

Db	2012	 TTCTCCAGGCGCAAGAAGAAGGGCAGCAAGCTGAAGAAGGCGCCAGCGTGGAGGAGGGA	2071
Qy	1786	GATGAGGGTCAGGACTCCCCGGGAGGCCAGAGCCGAGGGGCGACCCGGCAGAAGAAGACC	1845
Db	2072	 GATGAGGGTCAGGACTCCCCGGGAGGCCAGAGCCGAGGGGCGACCCGGCAGAAGAAGACC	2131
Qy	1846	ATGAAGCTGTCCCGGGCCCTCTCTGACCTGGTGAAGTACACCAAGTCCGTGGCCACCCAC	1905
Db	2132	 ATGAAGCTGTCCCGGGCCCTCTCTGACCTGGTGAAGTACACCAAGTCCGTGGCCACCCAC	2191
Qy	1906	GACATAGAGATGGAGGCGGCGTCCAGCTGGCAGGTGTCGTCTTCAGCGAGACCAAGGCC	1965
Db	2192	 GACATAGAGATGGAGGCGGCGTCCAGCTGGCAGGTGTCGTCTTCAGCGAGACCAAGGCC	2251
Qy	1966	CACCAGATTCTGCAGCAGAAGCCGGCGCAGTACCTACGCTTCAACCAGCAGCAGCTCTCC	2025
Db	2252	 CACCAGATTCTGCAGCAGAAGCCGGCGCAGTACCTACGCTTCAACCAGCAGCAGCTCTCC	2311
Qy	2026	CGCATCTACCCCTCCTCCTACCGTGTGGACTCCAGCAACTACAACCCGAGCCCTTCTGG	2085
Db	2312	 CGCATCTACCCCTCCTCCTACCGTGTGGACTCCAGCAACTACAACCCGAGCCCTTCTGG	2371
Qy	2086	AACGCCGGCTGCCAAATGGTTGCCCTGAACTACCAGTCAGAGGGGCGGATGCTGCAGCTG	2145
Db	2372	 AACGCCGGCTGCCAAATGGTTGCCCTGAACTACCAGTCAGAGGGGCGGATGCTGCAGCTG	2431
Qy	2146	AACCGAGCCAAGTTCAGCGCCAACGGTGGCTGCGGCTACGTACTCAAGCCTGGGTGCATG	2205
Db	2432	 AACCGAGCCAAGTTCAGCGCCAACGGTGGCTGCGGCTACGTACTCAAGCCTGGGTGCATG	2491
Qy	2206	TGCCAGGGCGTGTTCACCCCAACTCGGAGGACCCCTGCCCGGGCAGCTCAAGAAGCAG	2265
Db	2492	 TGCCAGGGCGTGTTCACCCCAACTCGGAGGACCCCTGCCCGGGCAGCTCAAGAAGCAG	2551
Qy	2266	CTGGTGCTCCGGATCATCAGTGGCCAGCAGCTTCCCAAGCCGCGCGACTCCATGCTGGGG	2325
Db	2552	 CTGGTGCTCCGGATCATCAGTGGCCAGCAGCTTCCCAAGCCGCGCGACTCCATGCTGGGG	2611
Qy	2326	GACCGTGGGGAGATCATCGACCCCTTTGTGGAGGTGGAGATCATTGGGCTCCCTGTGGAC	2385
Db	2612	 GACCGTGGGGAGATCATCGACCCCTTTGTGGAGGTGGAGATCATTGGGCTCCCTGTGGAC	2671
Qy	2386	TGCAGCAGGGAGCAGACCCGCGTGGTGGACGACAACGGGTTCAACCCACCTGGGAGGAG	2445
Db	2672	 TGCAGCAGGGAGCAGACCCGCGTGGTGGACGACAACGGGTTCAACCCACCTGGGAGGAG	2731
Qy	2446	ACCCTGGTTTTTCATGGTGCACATGCCGAGATCGCGTGGTCCGCTTCCTCGTCTGGGAC	2505
Db	2732	 ACCCTGGTTTTTCATGGTGCACATGCCGAGATCGCGTGGTCCGCTTCCTCGTCTGGGAC	2791
Qy	2506	CACGATCCCATCGGGCGTGACTTCATTGGCCAGAGGACGCTGGCCTTCAGCAGCATGATG	2565
Db	2792	 CACGATCCCATCGGGCGTGACTTCATTGGCCAGAGGACGCTGGCCTTCAGCAGCATGATG	2851
Qy	2566	CCAGGCTACAGACACGTGTACCTAGAAGGGATGGAAGAGGCTCCATCTTCGTGCATGTG	2625
Db	2852	 CCAGGCTACAGACACGTGTACCTAGAAGGGATGGAAGAGGCTCCATCTTCGTGCATGTG	2911
Qy	2626	GCTGTCAGTGACATCAGCGGTAAGGTCAAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTC	2685

Db	2912	GCTGTCAGTGACATCAGCGGTAAGGTCAAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTC	2971
Qy	2686	CGAGGCCCAAAGCCCGGCTCGCTGGACAGTCATGCTGCTGGGCGGCCCCCGGCCCGGCC	2745
Db	2972	CGAGGCCCAAAGCCCGGCTCGCTGGACAGTCATGCTGCTGGGCGGCCCCCGGCCCGGCC	3031
Qy	2746	TCCGTTAGCCAGCGGATCCTGCGGCGCACGGCCAGCGCCCGACCAAGAGCCAGAAGCCG	2805
Db	3032	TCCGTTAGCCAGCGGATCCTGCGGCGCACGGCCAGCGCCCGACCAAGAGCCAGAAGCCG	3091
Qy	2806	GGCCGCAGGGGCTTCCCGGAGCTGGTCTGGGTACACGGGACACAGGCTCCAAGGGGGTG	2865
Db	3092	GGCCGCAGGGGCTTCCCGGAGCTGGTCTGGGTACACGGGACACAGGCTCCAAGGGGGTG	3151
Qy	2866	GCAGACGATGTGGTGCCCCCGGGCCCGGACCTGCTCCGGAAGCCCCAGCCCAGGAGGGG	2925
Db	3152	GCAGACGATGTGGTGCCCCCGGGCCCGGACCTGCTCCGGAAGCCCCAGCCCAGGAGGGG	3211
Qy	2926	CCCGGCAGCGGCAGCCCCCGAG	2947
Db	3212	CCCGGCAGCGGCAGCCCCCGAG	3233

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	3624	100.0	3624	3	US-09-927-112-3	Sequence 3, Appli
2	3624	100.0	4635	3	US-09-927-112-1	Sequence 1, Appli
3	308.6	8.5	2289	3	US-10-258-860-1	Sequence 1, Appli
4	301.8	8.3	2211	3	US-09-800-971-3	Sequence 3, Appli
5	301.8	8.3	3425	3	US-09-800-971-1	Sequence 1, Appli
6	289.8	8.0	2627	4	US-09-880-107-3293	Sequence 3293, Ap
7	286.6	7.9	2752	3	US-10-104-047-135	Sequence 135, App
8	278.8	7.7	2627	3	US-09-949-016-5110	Sequence 5110, Ap
9	276.2	7.6	2462	3	US-10-258-860-5	Sequence 5, Appli
10	276.2	7.6	2540	3	US-10-258-860-3	Sequence 3, Appli
11	212.8	5.9	2958	3	US-09-688-078-5	Sequence 5, Appli
12	201.2	5.6	4147	3	US-09-688-078-6	Sequence 6, Appli
13	200.8	5.5	3006	3	US-09-688-078-1	Sequence 1, Appli
14	200.8	5.5	3238	3	US-09-688-078-8	Sequence 8, Appli
15	194.4	5.4	4543	3	US-09-949-002-135	Sequence 135, App
16	194.4	5.4	185765	3	US-09-949-002-674	Sequence 674, App

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3624	100.0	3624	3	US-09-927-112-3	Sequence 3, Appli
2	3624	100.0	3624	9	US-10-784-089-3	Sequence 3, Appli
3	3624	100.0	4635	3	US-09-927-112-1	Sequence 1, Appli
4	3624	100.0	4635	9	US-10-757-262-37	Sequence 37, Appl
5	3624	100.0	4635	9	US-10-784-089-1	Sequence 1, Appli
6	3345.2	92.3	4941	8	US-10-467-248-15	Sequence 15, Appl
7	3269.2	90.2	4237	8	US-10-275-998-10	Sequence 10, Appl
8	2838.4	78.3	6551	8	US-10-362-628-12	Sequence 12, Appl
9	2358	65.1	5365	8	US-10-322-281-224	Sequence 224, App
10	1840	50.8	2243	8	US-10-332-426-10	Sequence 10, Appl
11	1412.6	39.0	1833	8	US-10-322-281-227	Sequence 227, App
12	1127	31.1	3283	7	US-10-108-260A-1395	Sequence 1395, Ap
13	1111.2	30.7	3433	8	US-10-398-663-9	Sequence

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	2358	65.1	5365	6	US-10-539-228-224	Sequence 224, App
2	1412.6	39.0	1833	6	US-10-539-228-227	Sequence 227, App
3	1127	31.1	3283	8	US-11-293-697-1395	Sequence 1395, Ap
4	1103	30.4	3585	8	US-11-266-748A-32259	Sequence 32259, A
5	571.2	15.8	715	8	US-11-266-748A-366378	Sequence 366378,
c 6	571.2	15.8	715	8	US-11-266-748A-449757	Sequence 449757,
7	535.4	14.8	80105	6	US-10-539-228-223	Sequence 223, App
c 8	464.4	12.8	513	8	US-11-266-748A-104368	Sequence 104368,
9	464.4	12.8	513	8	US-11-266-748A-157179	Sequence 157179,
10	308.6	8.5	3107	8	US-11-266-748A-30946	Sequence 30946, A
11	308.6	8.5	3107	8	US-11-266-748A-56285	Sequence 56285, A
12	301.8	8.3	3445	8	US-11-266-748A-28175	Sequence 28175, A
13	301.8	8.3	5926	8	US-11-266-748A-22592	Sequence 22592, A
14	300.2	8.3	2773	8	US-11-266-748A-57630	Sequence 57630, A
15	244.4	6.7	43865	6	US-10-539-228-226	Sequence

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2548	70.3	5324	6	AK044619	AK044619	Mus muscu
2	1307.6	36.1	1836	6	AK049970	AK049970	Mus muscu
3	1170.6	32.3	1817	6	AK078731	AK078731	Mus muscu
4	920.2	25.4	947	14	DQ035829	DQ035829	Homo sapi
5	808	22.3	1278	14	DQ035827	DQ035827	Homo sapi
6	717.4	19.8	857	14	DQ035830	DQ035830	Pan trogl
7	693.8	19.1	886	10	DV878798	DV878798	LB0263.CR
8	669.2	18.5	692	8	CR998048	CR998048	CR998048
9	647	17.9	889	3	BQ946757	BQ946757	AGENCOURT
10	644.6	17.8	958	3	BU159213	BU159213	AGENCOURT
11	627	17.3	759	5	CF531476	CF531476	UI-M-FY0-
12	626.6	17.3	763	5	CF531795	CF531795	UI-M-FY0-
13	620	17.1	1092	3	BU502871	BU502871	AGENCOURT
14	610.4	16.8	930	3	BQ960462	BQ960462	AGENCOURT

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3624	100.0	4635	6	AAD39663	Aad39663 Human pho
2	3624	100.0	4635	13	ADQ89085	Adq89085 Human uro
3	3345.2	92.3	4941	6	ABV72132	Abv72132 Nucleotid
4	3269.2	90.2	4237	6	ABA96005	Aba96005 Human lip
5	2838.4	78.3	6551	6	ABK12390	Abk12390 cDNA enco
6	2838.4	78.3	6551	12	ADK70341	Adk70341 Respirato
7	2358	65.1	5365	13	ABD33214	Abd33214 Murine ca
8	1840	50.8	2243	6	ABA94696	Aba94696 Human lip
9	1412.6	39.0	1833	13	ABD33216	Abd33216 Human can
10	1127	31.1	3283	11	ADM02710	Adm02710 Human cDN
11	1127	31.1	3283	14	AEC85640	Aec85640 Human cDN
12	1111.2	30.7	3433	6	ABL60537	Abl60537 Human

SEQ ID 10: 2

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	6379	100.0	1207	5	AAE24599	Aae24599 Human pho
2	6379	100.0	1207	8	ADQ89086	Adq89086 Human uro
3	6092.5	95.5	1239	5	ABB08205	Abb08205 Human lip
4	5847.5	91.7	1152	5	ABB78295	Abb78295 Amino aci
5	5000	78.4	1605	8	ABO84827	Abo84827 Murine ca
6	4941	77.5	1619	5	AAU77498	Aau77498 Human lip
7	4941	77.5	1619	8	ADK70467	Adk70467 Respirato
8	3225	50.6	621	5	ABB07493	Abb07493 Human lip
9	3163	49.6	1014	5	ABB08001	Abb08001 Human lip
10	3161.5	49.6	968	7	ADM05153	Adm05153 Human pro
11	3161.5	49.6	968	9	AEC88083	Aec88083 Human cDN
12	2640	41.4	916	7	ADE47776	Ade47776 Human NOV
13	2640	41.4	916	8	ADJ79046	Adj79046 Human NOV
14	2343	36.7	787	4	ABG13669	Abg13669 Novel hum
15	2343	36.7	787	5	AAE14673	Aae14673 Human pho
16	2343	36.7	787	8	ADL61315	Adl61315 Human pro
17	2343	36.7	787	8	ADQ19653	Adq19653 Human sof

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	6379	100.0	1207	2	US-09-927-112-2	Sequence 2, Appli
2	1738	27.2	325	2	US-09-927-112-10	Sequence 10, Appl
3	1578	24.7	1154	2	US-09-688-078-7	Sequence 7, Appli
4	1563.5	24.5	1001	2	US-09-688-078-2	Sequence 2, Appli
5	1526.5	23.9	1017	2	US-09-949-002-421	Sequence 421, App
6	1524.5	23.9	997	2	US-09-961-403-15	Sequence 15, Appl
7	1524.5	23.9	997	2	US-09-949-002-388	Sequence 388, App
8	1517.5	23.8	916	2	US-09-688-078-9	Sequence 9, Appli
9	1441	22.6	762	2	US-10-258-860-2	Sequence 2, Appli
10	1385.5	21.7	759	2	US-10-258-860-6	Sequence 6, Appli
11	1372.5	21.5	785	2	US-10-258-860-4	Sequence 4, Appli
12	1290.5	20.2	777	2	US-10-104-047-2105	Sequence 2105, Ap
13	1281	20.1	744	2	US-09-738-884-4	Sequence

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	6379	100.0	1207	3	US-09-927-112-2	Sequence 2, Appli
2	6379	100.0	1207	4	US-10-757-262-38	Sequence 38, Appl
3	6379	100.0	1207	5	US-10-784-089-2	Sequence 2, Appli
4	6092.5	95.5	1239	4	US-10-275-998-5	Sequence 5, Appli
5	5847.5	91.7	1152	4	US-10-467-248-6	Sequence 6, Appli
6	4981	78.1	1601	4	US-10-322-281-225	Sequence 225, App
7	4941	77.5	1619	4	US-10-362-628-6	Sequence 6, Appli
8	3225	50.6	621	4	US-10-332-426-2	Sequence 2, Appli
9	3163	49.6	1014	4	US-10-398-663-1	Sequence 1, Appli
10	3161.5	49.6	968	4	US-10-108-260A-3838	Sequence 3838, Ap
11	2640	41.4	916	4	US-10-210-130-138	Sequence 138, App
12	2343	36.7	787	4	US-10-648-593-239	Sequence 239, App
13	2343	36.7	787	5	US-10-723-860-2472	Sequence 2472, Ap
14	2343	36.7	787	5	US-10-756-149-5375	Sequence 5375, Ap
15	2343	36.7	787	5	US-10-450-763-44028	Sequence 44028, A
16	2343	36.7	787	6	US-11-072-175-239	Sequence 239, App

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4981	78.1	1601	6	US-10-539-228-225	Sequence 225, App
2	3161.5	49.6	968	7	US-11-293-697-3838	Sequence 3838, Ap
3	1626.5	25.5	316	6	US-10-539-228-228	Sequence 228, App
4	997	15.6	1291	7	US-11-346-759-78	Sequence 78, Appl
5	955.5	15.0	1163	6	US-10-539-228-802	Sequence 802, App
6	927	14.5	1010	6	US-10-539-228-804	Sequence 804, App
7	900	14.1	1234	6	US-10-505-928-654	Sequence 654, App
8	840.5	13.2	1809	6	US-10-370-959-67	Sequence 67, Appl
9	773	12.1	403	7	US-11-293-697-4438	Sequence 4438, Ap
10	740	11.6	1057	6	US-10-539-228-799	Sequence 799, App
11	734.5	11.5	648	7	US-11-277-204-24	Sequence 24, Appl
12	604.5	9.5	553	6	US-10-953-349-15163	Sequence 15163, A
13	604.5	9.5	578	6	US-10-953-349-15162	Sequence 15162, A
14	593.5	9.3	598	6	US-10-449-902-48510	Sequence 48510, A
15	580.5	9.1	598	6	US-10-449-902-42757	Sequence 42757, A
16	580	9.1	617	6	US-10-449-902-50297	Sequence

Database : PIR_80:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1524.5	23.9	997	1	I54390	phosphoinositide-s
2	1517	23.8	1096	1	S62358	inositol 1,4,5-tri
3	1459	22.9	764	1	S14113	1-phosphatidylinos
4	1358.5	21.3	753	2	JC8057	phospholipase C (E
5	1297	20.3	895	2	T32374	hypothetical prote
6	1287	20.2	745	1	PC4183	1-phosphatidylinos
7	1285	20.1	756	1	A55943	1-phosphatidylinos
8	1258	19.7	756	1	B28821	1-phosphatidylinos
9	1244	19.5	709	2	C28821	1-phosphatidylinos
10	1009	15.8	1291	2	S00666	1-phosphatidylinos
11	997.5	15.6	1290	2	A36466	1-phosphatidylinos
12	997	15.6	1176	1	A48047	phospholipase C (E
13	986	15.5	1236	1	A53970	1-phosphatidylinos
14	985	15.4	1290	2	A31317	1-phosphatidylinos
15	968.5	15.2	1265	2	A34163	1-phosphatidylinos
16	950.5	14.9	1252	2	S02004	phospholipase C (E
17	947.5	14.9	1312	1	B40879	phospholipase C (E
18	945	14.8	1216	2	A28821	1-phosphatidylinos
19	943	14.8	1305	2	A40879	phospholipase

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5893	92.4	1129	2	Q86YU9_HUMAN	Q86yu9 homo sapien
2	5852	91.7	1182	1	PLCL4_HUMAN	O75038 homo sapien
3	5576	87.4	1058	2	Q5TA87_HUMAN	Q5ta87 homo sapien
4	5149.5	80.7	1164	2	Q4QSC7_MOUSE	Q4qsc7 mus musculu
5	5047	79.1	1416	2	Q3LUA8_HUMAN	Q3lua8 homo sapien
6	4647.5	72.9	1501	2	Q3LUA7_MOUSE	Q3lua7 mus musculu
7	4113.5	64.5	1238	2	Q86XJ2_HUMAN	Q86xj2 homo sapien
8	3905.5	61.2	1168	2	Q5TA86_HUMAN	Q5ta86 homo sapien
9	3450	54.1	656	2	Q8TEH5_HUMAN	Q8teh5 homo sapien
10	3166.5	49.6	1682	2	Q4KWH5_MOUSE	Q4kwh5 mus musculu
11	3159.5	49.5	1002	2	Q4KWH9_HUMAN	Q4kwh9 homo sapien
12	3159.5	49.5	1693	2	Q4KWH8_HUMAN	Q4kwh8 homo sapien
13	3157	49.5	1003	2	Q4KWH7_MOUSE	Q4kwh7 mus musculu
14	3157	49.5	1073	2	Q4KWH6_MOUSE	Q4kwh6 mus

RESULT 1

Q86YU9_HUMAN

ID Q86YU9_HUMAN PRELIMINARY; PRT; 1129 AA.
AC Q86YU9;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE FLJ00414 protein (Fragment).
GN Name=FLJ00414;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = 1D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AK122589; BAC56930.1; -; mRNA.
DR HSSP; P10688; 1DJX.
DR Ensembl; ENSG00000149527; Homo sapiens.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR011992; EF-Hand_type.
DR InterPro; IPR002048; EF_hand_Ca_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH_type.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_X.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00036; efhand; 3.
DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD000012; EF-hand; 1.
DR ProDom; PD001202; PI_PLC_Y; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00054; EFh; 2.
DR SMART; SM00148; PLCXc; 1.
DR SMART; SM00149; PLCYc; 1.
DR PROSITE; PS50004; C2_DOMAIN; 1.
DR PROSITE; PS00018; EF_HAND_1; UNKNOWN_1.
DR PROSITE; PS50222; EF_HAND_2; 2.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.

DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 KW Calcium; Hydrolase; Lipid degradation; Transducer.
 FT NON_TER 1 1
 SQ SEQUENCE 1129 AA; 123498 MW; CBC23844616C5402 CRC64;

Query Match 92.4%; Score 5893; DB 2; Length 1129;
 Best Local Similarity 99.7%; Pred. No. 6.6e-276;
 Matches 1118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	87	ISIDSIQEVSEGRQSEVFQRYPDGSFDPNCCFSIYHGSHRESLDLVSTSEVARTWVTGL	146
		:	
Db	9	VSIDSIQEVSEGRQSEVFQRYPDGSFDPNCCFSIYHGSHRESLDLVSTSEVARTWVTGL	68
Qy	147	RYLMAGISDEDSLARRQRTRDQWLKQTFDEADKNGDGSLSIGEVQLLHKLNVNLPQRV	206
Db	69	RYLMAGISDEDSLARRQRTRDQWLKQTFDEADKNGDGSLSIGEVQLLHKLNVNLPQRV	128
Qy	207	KQMFREADTDDHQGTLGFEFCAFYKMMSTRRDLYLLMLTYSNHKDHLDAASLQRFLOVE	266
Db	129	KQMFREADTDDHQGTLGFEFCAFYKMMSTRRDLYLLMLTYSNHKDHLDAASLQRFLOVE	188
Qy	267	QKMAGVTLESCQDII EQFEPENKSKGLLGIDGFTNYTRSPAGDIFNPEHHHVHQMTO	326
Db	189	QKMAGVTLESCQDII EQFEPENKSKGLLGIDGFTNYTRSPAGDIFNPEHHHVHQMTO	248
Qy	327	PLSHYFITSSHNTYLVDQQLMSQSRVDMYAWVLQAGCRCVEVDCWDGPDGEPVHHGYTL	386
Db	249	PLSHYFITSSHNTYLVDQQLMSQSRVDMYAWVLQAGCRCVEVDCWDGPDGEPVHHGYTL	308
Qy	387	TSKILFKDVIETINKYAFIKNEYPVILSIENHCSVIQQKKMAQYLTDLGDKLDLSSVSS	446
Db	309	TSKILFKDVIETINKYAFIKNEYPVILSIENHCSVIQQKKMAQYLTDLGDKLDLSSVSS	368
Qy	447	EDATTLPSQMLKGKILVKGKKLPANISEDAAEEGEVSEDSADEIDDDCKLLNGDASTNR	506
Db	369	EDATTLPSQMLKGKILVKGKKLPANISEDAAEEGEVSEDSADEIDDDCKLLNGDASTNR	428
Qy	507	KRVENTAKRKLD SLIKESKIRDCEDPNNFVS VTLSPSGKLGRKSKAEEDVESGEDAGASR	566
Db	429	KRVENTAKRKLD SLIKESKIRDCEDPNNFVS VTLSPSGKLGRKSKAEEDVESGEDAGASR	488
Qy	567	RNGRLVVGFSFSRRKKKGSKLKKAA SVEEGDEGQDSPGGQSRGATRQKKTMKLSRALSDLV	626
Db	489	RNGRLVVGFSFSRRKKKGSKLKKAA SVEEGDEGQDSPGGQSRGATRQKKTMKLSRALSDLV	548
Qy	627	KYTKSVATHDI EMEAASSWQVSSFSETKAHQILQQKPAQYLRFNQQQLSRIYPSSYRVDS	686
Db	549	KYTKSVATHDI EMEAASSWQVSSFSETKAHQILQQKPAQYLRFNQQQLSRIYPSSYRVDS	608
Qy	687	SNYNPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSED	746
Db	609	SNYNPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSED	668
Qy	747	PLPGQLKKQLVLR IISGQQLPKPRDSMLGDRGEI IDPFVEVEI IGLPVDCSREQTRVDD	806
Db	669	PLPGQLKKQLVLR IISGQQLPKPRDSMLGDRGEI IDPFVEVEI IGLPVDCSREQTRVDD	728
Qy	807	NGFNPTWEETLVFMVHMPEIALVRFLVWDHDP IGRDFIGQRTLAFSSMMPGYRHVYLEGM	866
Db	729	NGFNPTWEETLVFMVHMPEIALVRFLVWDHDP IGRDFIGQRTLAFSSMMPGYRHVYLEGM	788

Qy	867	EEASIFVHVAVSDISGKVKQALGLKGLFLRGPKPGSLD SHAAGRPPARPSVQRILRRTA	926
Db	789	EEASIFVHVAVSDISGKVKQVLGLKGLFLRGPKPGSLD SHAAGRPPARPSVQRILRRTA	848
Qy	927	SAPTKSQKPGRRGFPPELVLTGTRDTGSKGVADDVVP GP GPAP EAPAQEGPGSGSPRGKAP	986
Db	849	SAPTKSQKPGRRGFPPELVLTGTRDTGSKGVADDVVP GP GPAP EAPAQEGPGSGSPRGKAP	908
Qy	987	AAVAEKS PVRVRPPRVL DGP G PAGMAATCMKCVVGS CAGVNTGGLQ RERPPSPGPASRQA	1046
Db	909	AAVAEKS PVRVRPLRVL DGP G PAGMAATCMKCVVGS CAGVNTGGLQ RERPPSPGPASRQA	968
Qy	1047	AIRQQPRARADSLGAPCCGLD PHAIPGRSREAPKGP GAWRQGP GSGSMS SSSPDSPG	1106
Db	969	AIRQQPRARADSLGAPCCGLD PHAIPGRSREAPKGP GAWRQGP GSGSMS SSSPDSPG	1028
Qy	1107	IPERSPRWPEGACRQPGALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPHAPGMA	1166
Db	1029	IPERSPRWPEGACRQPGALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPHAPGMA	1088
Qy	1167	GPGSPAAASAWTVSPRVLVLVALYPWHCLRGTLLPWLACGP	1207
Db	1089	GPGSPAAASAWTVSPRVLVLVALYPWHCLRGTLLPWLACGP	1129

RESULT 3

Q5TA87_HUMAN

ID Q5TA87_HUMAN PRELIMINARY; PRT; 1058 AA.

AC Q5TA87;

DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.

DT 21-DEC-2004, sequence version 1.

DT 07-FEB-2006, entry version 9.

DE Novel protein.

GN Name=RP3-395M20.1; ORFNames=RP3-395M20.1-001;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Moore M.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

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CC -----

DR EMBL; AL139246; CAI20407.1; -; Genomic_DNA.

DR Ensembl; ENSG00000149527; Homo sapiens.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; IEA.

DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR GO; GO:0006629; P:lipid metabolism; IEA.

DR InterPro; IPR000008; C2.

DR InterPro; IPR011992; EF-Hand_type.

DR InterPro; IPR002048; EF_hand_Ca_bd.

DR InterPro; IPR001192; PI_PLC.

DR InterPro; IPR000909; PI_PLC_X.

DR InterPro; IPR001711; PI_PLC_Y.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00036; efhand; 3.

DR Pfam; PF00388; PI-PLC-X; 1.

DR Pfam; PF00387; PI-PLC-Y; 1.

DR PRINTS; PR00360; C2DOMAIN.

DR PRINTS; PR00390; PHPLIPASEC.

DR ProDom; PD000012; EF-hand; 1.

DR ProDom; PD001202; PI_PLC_Y; 2.

DR SMART; SM00239; C2; 1.

DR SMART; SM00054; EFh; 2.

DR SMART; SM00148; PLCXc; 1.

DR SMART; SM00149; PLCYc; 1.

DR PROSITE; PS50004; C2_DOMAIN; 1.

DR PROSITE; PS00018; EF_HAND_1; UNKNOWN_1.

DR PROSITE; PS50222; EF_HAND_2; 2.

DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.

DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.

SQ SEQUENCE 1058 AA; 115520 MW; D923C4349BE6BD17 CRC64;

Query Match 87.4%; Score 5576; DB 2; Length 1058;

Best Local Similarity 100.0%; Pred. No. 1.2e-260;

Matches 1058; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 MAGISDEDSLARRQRTDQWLKQTFDEADKNGDGSLSIGEVQLLHKLNVNLPQRVKQM 209

|||||

Db 1 MAGISDEDSLARRQRTDQWLKQTFDEADKNGDGSLSIGEVQLLHKLNVNLPQRVKQM 60

Qy	210	FREADTDDHQGT	LGFE	EFCAF	YKMM	STRD	LYLL	MLTY	SNHK	DHLDA	ASLQ	RFLQ	VEQK	M	269
Db	61	FREADTDDHQGT	LGFE	EFCAF	YKMM	STRD	LYLL	MLTY	SNHK	DHLDA	ASLQ	RFLQ	VEQK	M	120
Qy	270	AGVTLESCQDI	IEQF	EPCP	ENKSK	GLLG	IDGF	TNYTR	SPAG	DIFN	PEHH	VHQD	MTQPL	S	329
Db	121	AGVTLESCQDI	IEQF	EPCP	ENKSK	GLLG	IDGF	TNYTR	SPAG	DIFN	PEHH	VHQD	MTQPL	S	180
Qy	330	HYFITSSHNTY	LVGD	QLMS	QSRV	DMYAW	VLQAG	CRCV	EVDC	WDGP	DGEPI	VHHG	YTLT	SK	389
Db	181	HYFITSSHNTY	LVGD	QLMS	QSRV	DMYAW	VLQAG	CRCV	EVDC	WDGP	DGEPI	VHHG	YTLT	SK	240
Qy	390	ILFKDVIETIN	KYAFI	KNEYP	VILSI	ENHCS	VIQK	KMAQ	YLT	DILG	DKLD	SSVS	SEDA		449
Db	241	ILFKDVIETIN	KYAFI	KNEYP	VILSI	ENHCS	VIQK	KMAQ	YLT	DILG	DKLD	SSVS	SEDA		300
Qy	450	TTLPSQMLKGI	LVKG	KKLP	ANIS	EDAEE	GEVS	DEDS	ADEI	DDCK	LLNG	DAST	NRKR	V	509
Db	301	TTLPSQMLKGI	LVKG	KKLP	ANIS	EDAEE	GEVS	DEDS	ADEI	DDCK	LLNG	DAST	NRKR	V	360
Qy	510	ENTAKRKLD	SLIKE	SKIRD	CEDP	NNFS	VSTLS	PSGK	LGRK	SKAE	EDVE	SGED	AGAS	RRNG	569
Db	361	ENTAKRKLD	SLIKE	SKIRD	CEDP	NNFS	VSTLS	PSGK	LGRK	SKAE	EDVE	SGED	AGAS	RRNG	420
Qy	570	RLVVGFS	SRRKK	KGSK	LKKA	ASVE	EGDE	GQDS	PGGQ	SRGAT	RQKKT	MKLS	RALS	DLVK	YT 629
Db	421	RLVVGFS	SRRKK	KGSK	LKKA	ASVE	EGDE	GQDS	PGGQ	SRGAT	RQKKT	MKLS	RALS	DLVK	YT 480
Qy	630	KSVATHD	IEMEA	ASSW	QVSF	SETK	AHQIL	QKPA	QYLR	FNQQ	LSRI	YPSS	YRVD	SSNY	689
Db	481	KSVATHD	IEMEA	ASSW	QVSF	SETK	AHQIL	QKPA	QYLR	FNQQ	LSRI	YPSS	YRVD	SSNY	540
Qy	690	NPQPFWNAG	CQMV	ALNY	QSEGR	MLQL	NRAK	FSAN	GGCG	YVLK	PGCM	CQGV	FNPN	SEDPLP	749
Db	541	NPQPFWNAG	CQMV	ALNY	QSEGR	MLQL	NRAK	FSAN	GGCG	YVLK	PGCM	CQGV	FNPN	SEDPLP	600
Qy	750	GQLKKQLVL	RIIS	GQQL	PKPR	DSML	GDRGE	IIDP	FVEVE	IIGL	PVDC	SREQ	TRVVD	DNNGF	809
Db	601	GQLKKQLVL	RIIS	GQQL	PKPR	DSML	GDRGE	IIDP	FVEVE	IIGL	PVDC	SREQ	TRVVD	DNNGF	660
Qy	810	NPTWEETLV	FVMH	MP	PEIA	LVRFL	VWDH	DP	IGRDF	IGQRT	LAFSS	MMPG	YRHY	LEGMEA	869
Db	661	NPTWEETLV	FVMH	MP	PEIA	LVRFL	VWDH	DP	IGRDF	IGQRT	LAFSS	MMPG	YRHY	LEGMEA	720
Qy	870	SIFVHVAVSD	ISGK	VKQ	ALGL	KGLF	LRGP	KPGS	LD	SHAAG	RPPAR	PSVS	QRI	LRRTASAP	929
Db	721	SIFVHVAVSD	ISGK	VKQ	ALGL	KGLF	LRGP	KPGS	LD	SHAAG	RPPAR	PSVS	QRI	LRRTASAP	780
Qy	930	TKSQKPGRR	GFPE	LVLG	TRDT	GSKG	VADD	VVPP	PGPG	PAPE	APAQ	EGPG	SGSP	RGKAPAAV	989
Db	781	TKSQKPGRR	GFPE	LVLG	TRDT	GSKG	VADD	VVPP	PGPG	PAPE	APAQ	EGPG	SGSP	RGKAPAAV	840
Qy	990	AEKSPVRVR	PPRV	LDG	PGP	AGMA	ATCM	KCVG	SCAG	VNTG	GLQR	ERPP	SPGP	ASRQAAIR	1049
Db	841	AEKSPVRVR	PPRV	LDG	PGP	AGMA	ATCM	KCVG	SCAG	VNTG	GLQR	ERPP	SPGP	ASRQAAIR	900
Qy	1050	QQPRARADSL	GAPC	CGLD	PHAIP	GRSRE	APKGP	GAWR	QGP	GGSG	SMSS	DSSS	PDSP	GIPE	1109
Db	901	QQPRARADSL	GAPC	CGLD	PHAIP	GRSRE	APKGP	GAWR	QGP	GGSG	SMSS	DSSS	PDSP	GIPE	960
Qy	1110	RSPRWPEGAC	RQPG	ALQ	GEMSA	LFAQ	KLEE	IRSK	SPMF	SAGK	PLLPC	VVLPH	APGM	AGPG	1169

```

          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 RSPRWPEGACRQPGALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPHPAGMAGPG 1020
Qy      1170 SPAAASAWTVSPRVLVLVALYPWHCLRGTTLLPWLACGP 1207
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 SPAAASAWTVSPRVLVLVALYPWHCLRGTTLLPWLACGP 1058
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